

Fig 1

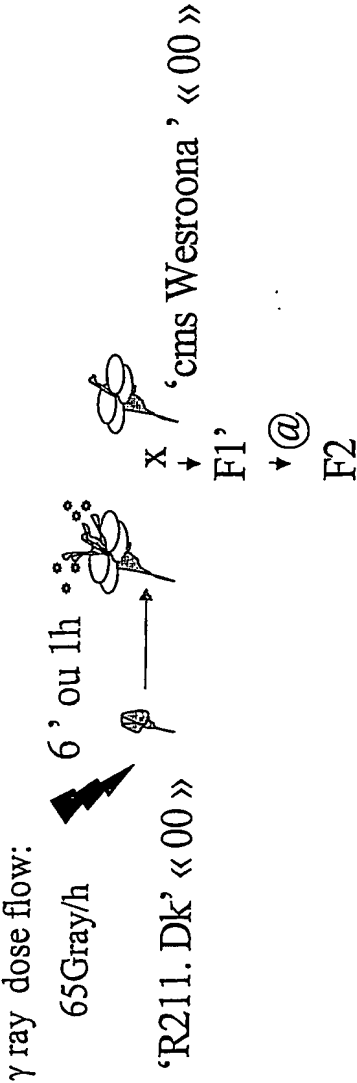


Fig 2

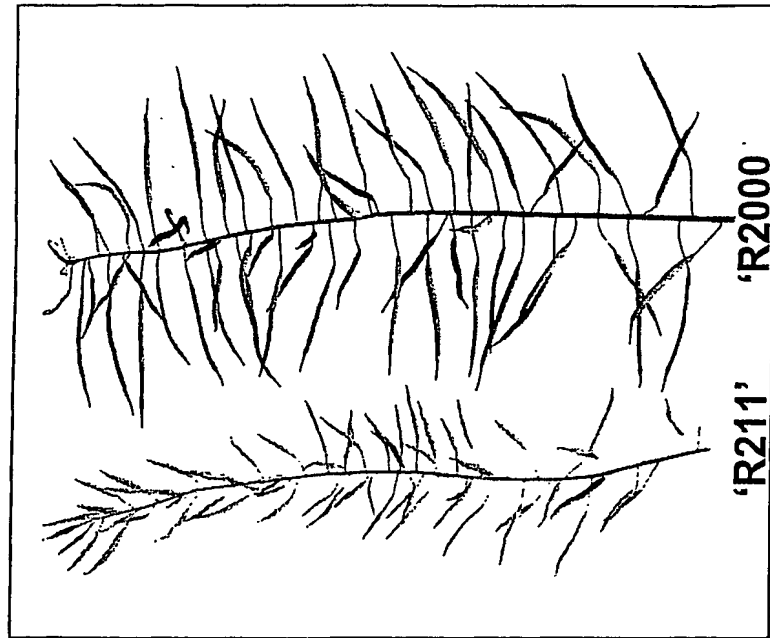


Fig. 1: Seed set on 'R211' and 'R2000'

Fig 3

| Genotype | Selfings           | Test Crosses               |
|----------|--------------------|----------------------------|
| Drakkar  | 29.3               | 25.5<br>27.0 (24.0 – 28.7) |
| Pactol   | 23.1               |                            |
| R211     | 11.2               |                            |
| R2000    | 26.5 (24.0 – 31.1) |                            |

[illegible]

Fig 5

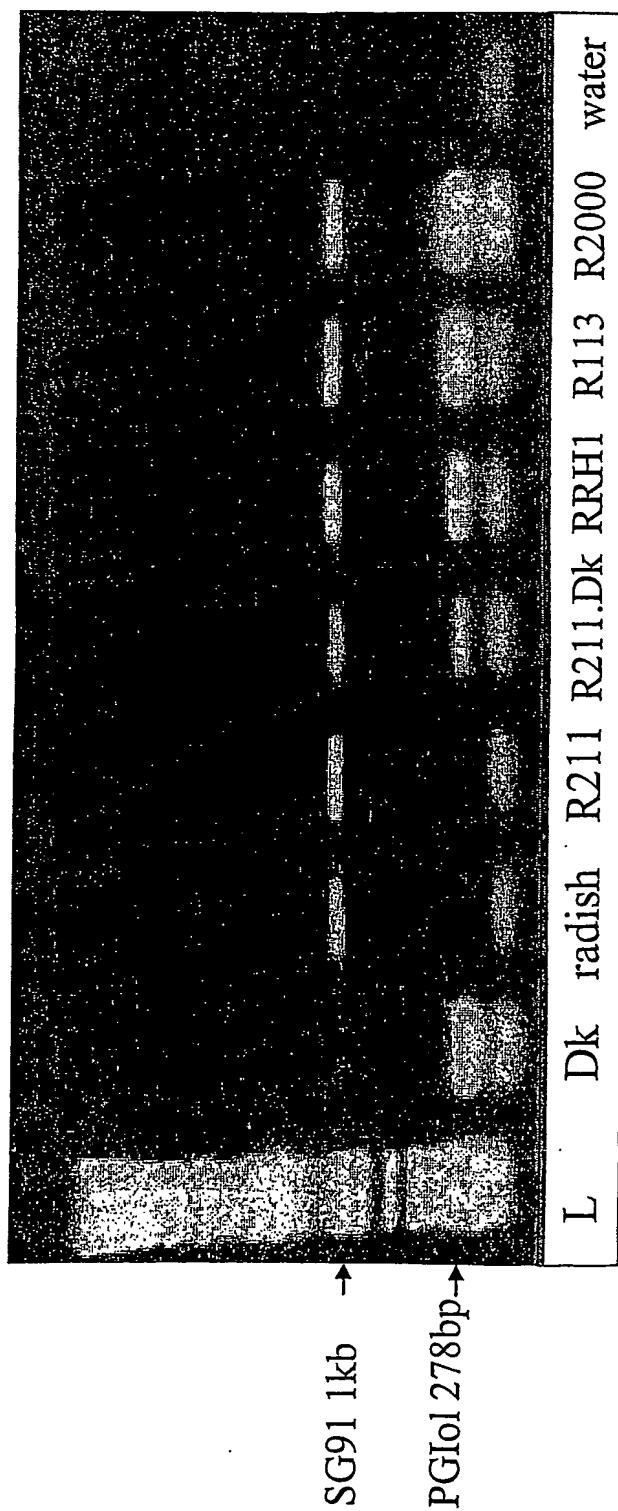


Fig 6

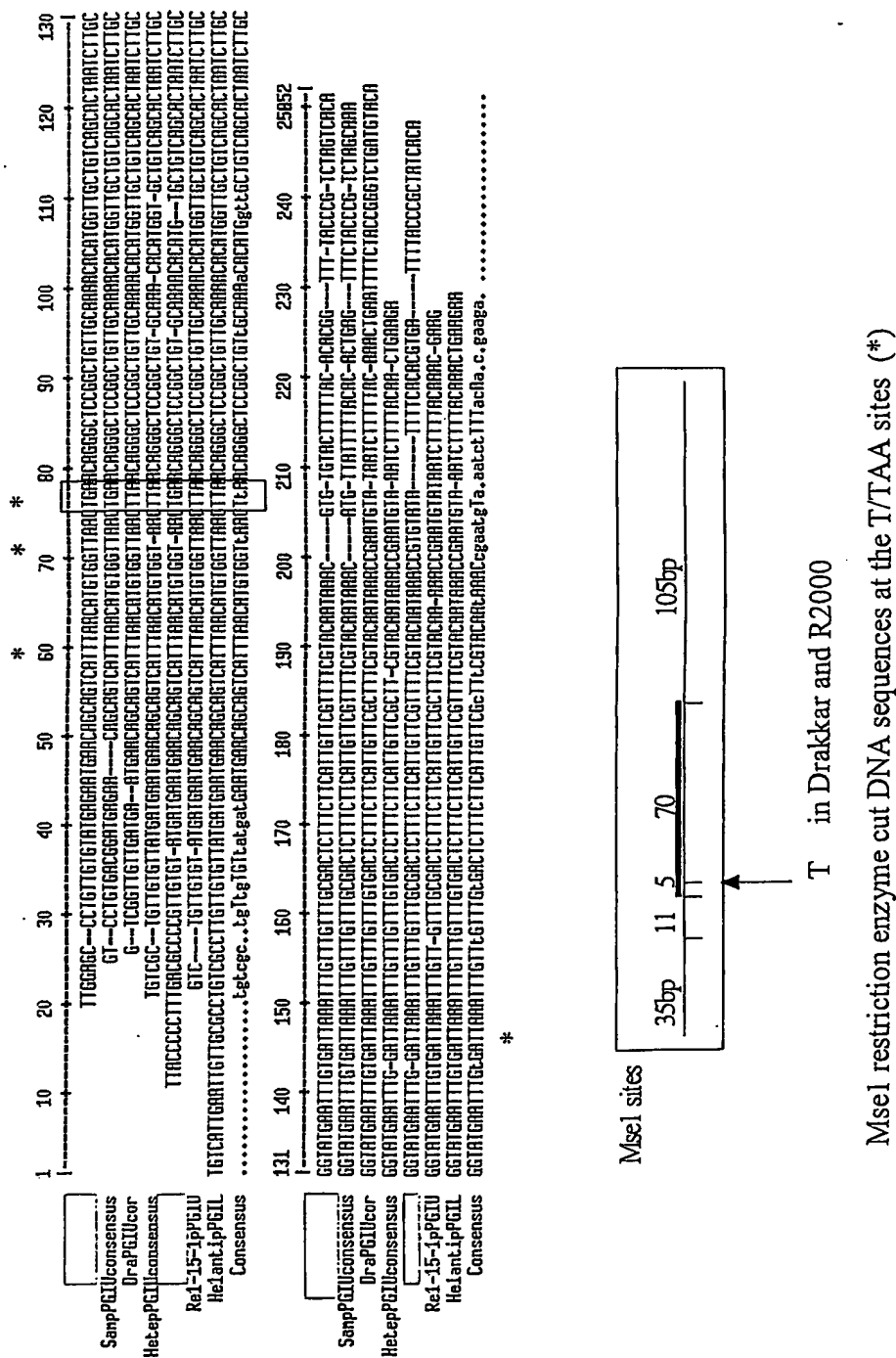


Fig 7

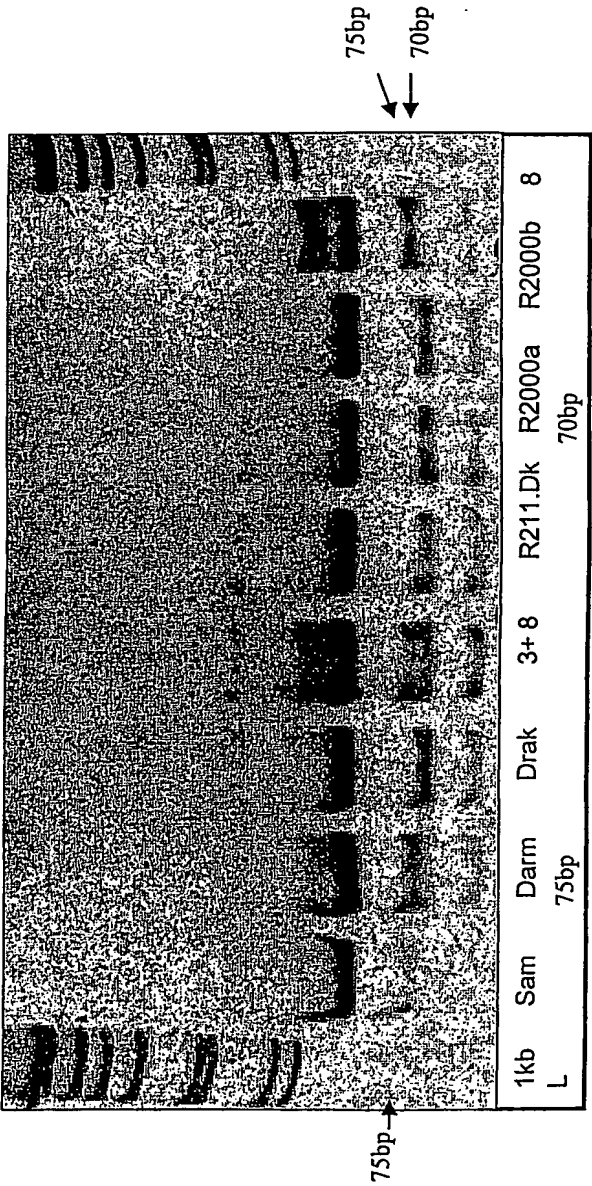


Fig 8

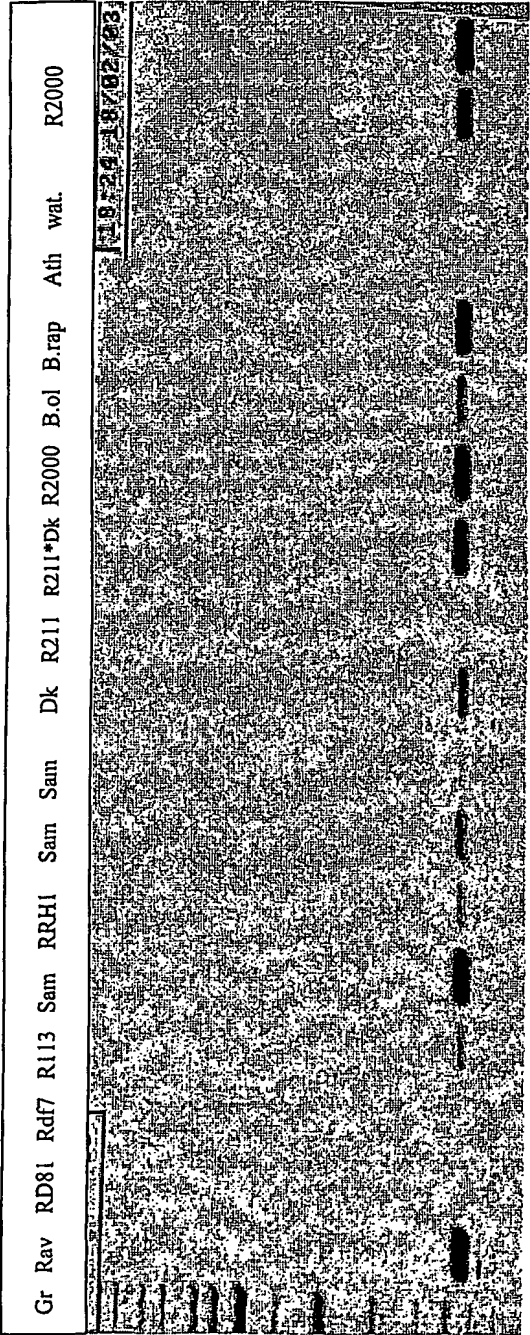




Fig 9

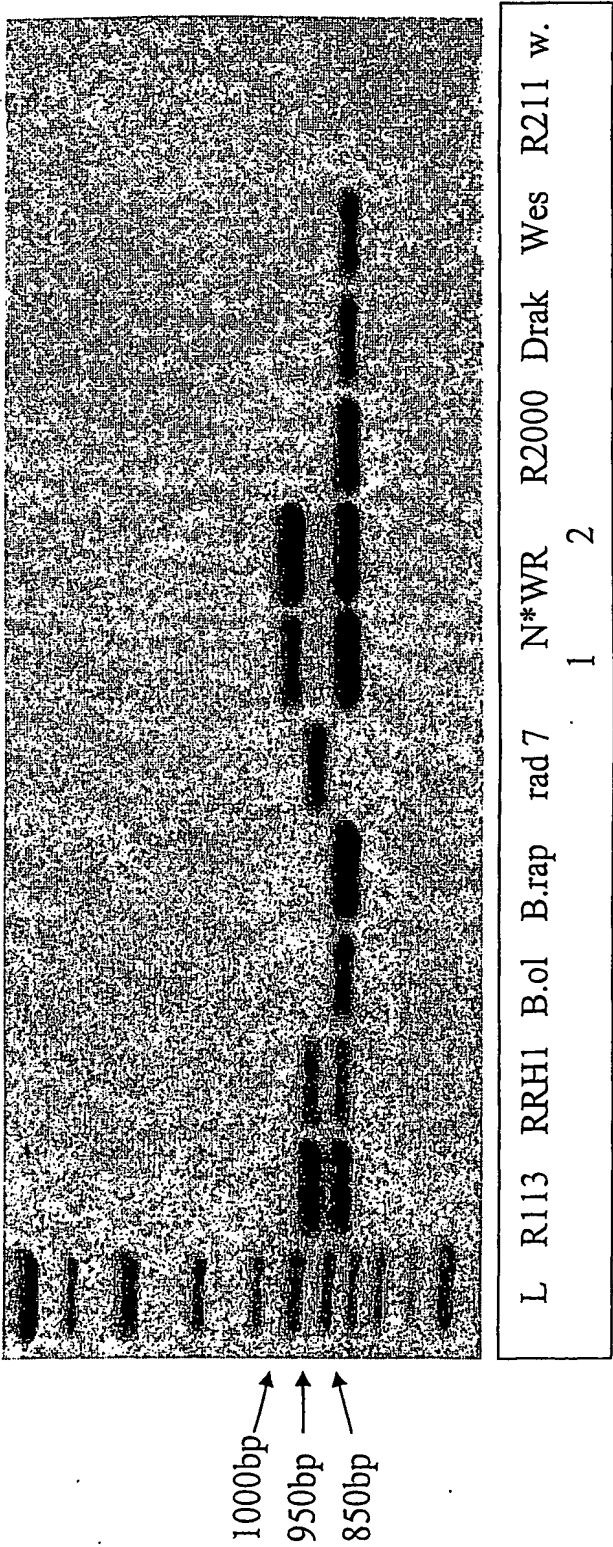


Fig 10

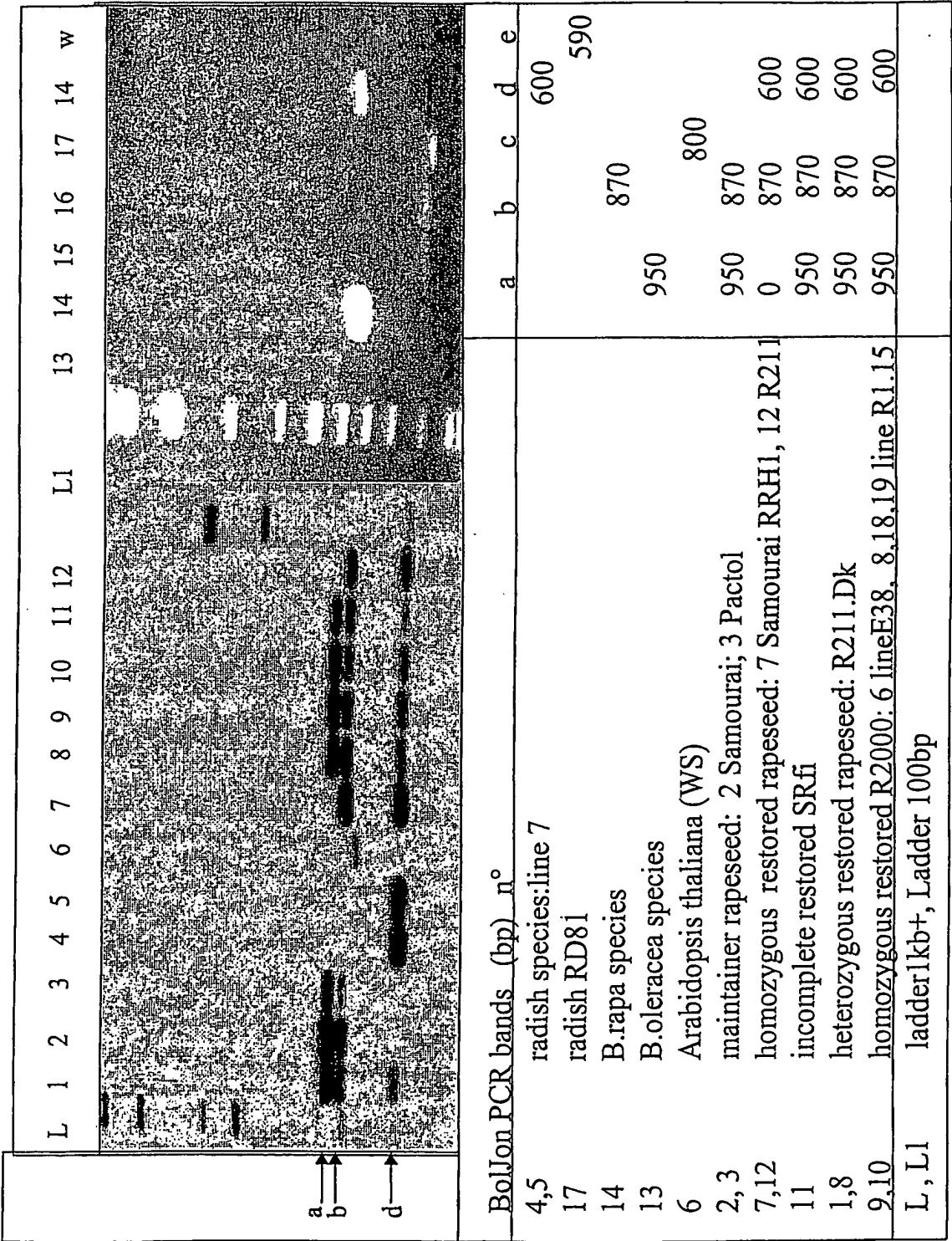
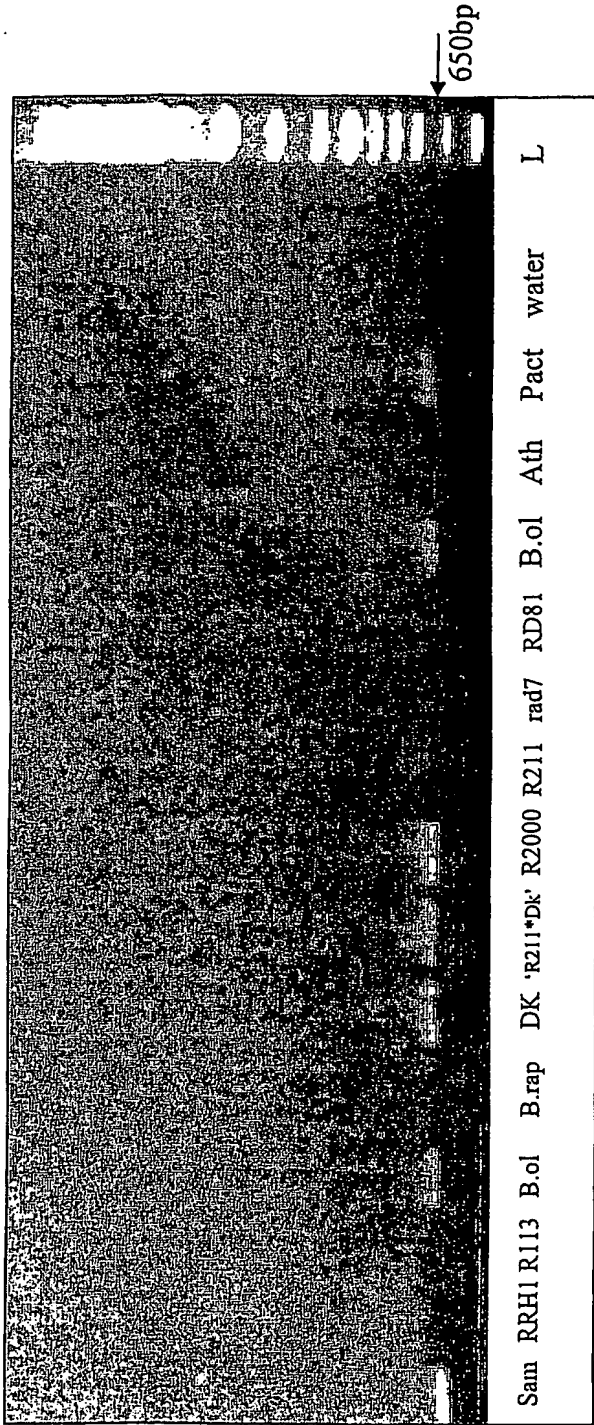


Fig 11



The CP418 band (about 650bp) specific to the *B.oleracea* genome.  
It is present in B.ol, B.napus (Samourai, Drakkar, Pactol and the herterozygous R211\*Dk)  
It is absent from the restored rapeseed (RRH, R113 and R211)  
It is present in the homozygous R2000.



Figure 13 (a)

|                      |             |                |                         |                                  |
|----------------------|-------------|----------------|-------------------------|----------------------------------|
|                      | 51          |                | 81 PGIol U -->          | 100                              |
| consePGIintUNTDrakka | .....       | .....          | .....                   | .....                            |
| consensWesrPGI       | .....       | .....          | .....                   | .....                            |
| consePGIintUNTR113   | .....       | .....          | .....                   | .....                            |
| consePGIintUNTBrapaA | .....       | .....          | .....                   | .....                            |
| ConsePGIintUNTRRH1   | .....       | .....          | .....                   | .....                            |
| PGIBo-EM:AF258277    | TTGCTTAGCG  | TCCAAATTTC     | ATGATTGTAT              | TCATTTGATT GTTGTG....            |
| PGIBra-EM:AF258278   | TTGCTTAGCG  | TCCAAATTTC     | ATGATTGTAT              | TCATTTGATT GTTGTGTGAC            |
| consePGIintUNTBolera | .....       | .....          | .....                   | .....                            |
| consePGIintUNTR2000  | .....       | .....TTG...    | TCATT.GA...TTGT.TGCC    | 1                                |
| Consensus            |             |                |                         |                                  |
|                      | 101         | ----           |                         | 150                              |
| consePGIintUNTDrakka | .....       | .....GTCG      | TTTGTGTTGGTG            | AGT.GAACAG CAGTCATTTA            |
| consensWesrPGI       | .....       | .....GCCTGTTTG | TGTTATGATG              | AAT.GAACAG CAGTCATTTA            |
| consePGIintUNTR113   | .....       | .....GCCCGTTG  | .....G                  | TAT.GAAACG CAG.CATTTA            |
| consePGIintUNTBrapaA | .....       | .....          | .....G                  | CAGTCATTTA                       |
| ConsePGIintUNTRRH1   | .....       | .....          | .....CG                 | TGTTGAGAAG CAG.CATTTA            |
| PGIBo-EM:AF258277    | .....       | CTG            | TCGCCCTGTTG             | TGTTA.GATG AAT.GAACAG CAGTCATTTA |
| PGIBra-EM:AF258278   | .....       | TATCGCCTC.     | TCGCCCTGTTG             | TGTTATGATG AAT.GAACAG CAGTCATTTA |
| consePGIintUNTBolera | .....       | .....          | .....                   | .....                            |
| consePGIintUNTR2000  | .....       | CTG            | TCGCCCTGTTG             | TGTTATGATG AAT.GAACA. CAGTCATTTA |
| Consensus            | .....       | ....           | .....t.g                | .....g ...t.gaa.ag cagtcattta    |
|                      | 151         |                | * MseI restriction site | 200                              |
| consePGIintUNTDrakka | ACATG.TGGT  | TAAC           | TAACA GGGCTCCGGC        | TGTTGCAAAA CACATGGTTG            |
| consensWesrPGI       | ACATG.TGGT  | TAAC           | TAACA GGGCTCCGGC        | TGTTGCAAAA CACATGGTTG            |
| consePGIintUNTR113   | ACATG.TGGT  | .AACTGAACA     | GGGCTCCGGC              | TGTTGCC...CTAAGGGTTG             |
| consePGIintUNTBrapaA | ACATGGTGGT  | TAAC           | TAACA GGGCTCCGGC        | TGTTGCAAAA CACATGGTTG            |
| ConsePGIintUNTRRH1   | ACATG..GGT  | .ACTGAACA      | GGGC.CCGGC              | TGTTGCAA...ACAG...TG             |
| PGIBo-EM:AF258277    | ACATG.TGGT  | TAAC           | TAACA GGGCTCAGGC        | TGTTGCAAAA CACATGGTTG            |
| PGIBra-EM:AF258278   | ACATG.TGGT  | TAAC           | TAACA GGGCTCCGGC        | TGTTGCAAAA CATATGGTTG            |
| consePGIintUNTBolera | .....       | .....          | .....C                  | TGTTGCAAAA CACATGGTTG            |
| consePGIintUNTR2000  | ACATG.TGGT  | TAAC           | TAACA GGGCTCCGGC        | TGTTGCAAAA CACATGGTTG            |
| Consensus            | acatg.tggt  | taact.         | taaca gggctccggc        | tggtgcaaaa cacatggttg            |
|                      | 201         |                | PGI int U ---->         | 250                              |
| consePGIintUNTDrakka | CTGT        | CAGCAC         | TAATCTTGC GGTATG        | AATT TGTGATTAAA TTTGTTTGT        |
| consensWesrPGI       | CTGT        | CAGCAC         | TAATCTTGC GGTATG        | AATT TGTGATTAAA TTTGTTTGT        |
| consePGIintUNTR113   | CTGT        | CAGCAC         | TAATCTTGC GGTATG        | AATT TGTGATTAAA TTTGTTTGT        |
| consePGIintUNTBrapaA | CTGT        | CAGCAC         | TAATCTTGC GGTATG        | AATT TGTGATTAAA TTTGTTTGT        |
| ConsePGIintUNTRRH1   | CTGT        | CAGCAC         | TAATCTTGC GGTATG        | AATT TGTGATTAAA TTTGTTTGT        |
| PGIBo-EM:AF258277    | CTGT        | CAGCAC         | TAATCTTGC GGTATG        | AATT TGTGATTAAA TTTGTTTGT        |
| PGIBra-EM:AF258278   | CTGT        | CAGCAC         | TAATCTTGC GGTATG        | AATT TGTGATTAAA TTTGTTTGT        |
| consePGIintUNTBolera | CTGT        | CAGCAC         | TAATCTTGC GGTATG        | AATT TGTGATTAAA TTTGTTTGT        |
| consePGIintUNTR2000  | CTGT        | CAGCAC         | TAATCTTGC GGTATG        | AATT TGTGATTAAA TTTGTTTGT        |
| Consensus            | ctgtcagcac  | taatcttgc      | ggtatg aatt             | tgtgattaaa tttgtttgt             |
|                      | 251         |                |                         | 300                              |
| consePGIintUNTDrakka | TGTGACTCTT  | T.CTTTCATTG    | TTCGTTTTTCG             | TACAATAAAC CGAATGTATA            |
| consensWesrPGI       | TGTGACTCTT  | T.CTTTCATTG    | TTCGTTTTTCG             | TACAATAAAC CGAATGTATA            |
| consePGIintUNTR113   | TGCGACTCTT  | T.CTTTCATTG    | TTCGTTTTTCG             | TACAATAAAC ..AATGTATA            |
| consePGIintUNTBrapaA | TGCGACTCTT  | T.CTTTCATTG    | TTCGTTTTTCG             | TACAATAAAC ..AATGTATA            |
| ConsePGIintUNTRRH1   | TGCGACTCTT  | T.CTTTCATTG    | TTCGTTTTTCG             | TACAATAAAC ..AATGTATA            |
| PGIBo-EM:AF258277    | TGTGACTCTT  | T.CTTTCATTG    | TTCGTTTTTCG             | TACAATAAAC CGAATGTATA            |
| PGIBra-EM:AF258278   | TGTGACTCTT  | T.CTTTCATTG    | TTCGTTTTTCG             | TACAATAAAC CGAATGTATA            |
| consePGIintUNTBolera | TG.GACTCTT  | T.CTTTCATTG    | TTCGTTTTTCG             | TACAATAAAC CGAATGTATA            |
| consePGIintUNTR2000  | TGTGACTCTT  | T.CTTTCATTG    | TTCGTTTTTCG             | TACAATAAAC CGAATGTATA            |
| Consensus            | tg.gactcctt | t.cttccattg    | ttcgtttttcg             | tacaataaac cgaatgtata            |

Figure 13 (b)

|                      | 301                  | <---                       | PGIol antL 341 | 350 |
|----------------------|----------------------|----------------------------|----------------|-----|
| consePGIintUNTDrakka | ATCTTTTTAC AAAC TGAA | TT TTCTACCGGG TCTGATGTAC A | ATGCTAGTC      |     |
| consensWesrPGI       | ATCTTTTTAC AAAC TGAA | TT TTCTACCGGG TCTGATGTAC A | ATGCTAGTC      |     |
| consePGIintUNTR113   | ATCTTTTTAC AAAC TGAA | TT TTCTACCGGG TCTGATGTAC A | ATGCTAGTC      |     |
| consePGIintUNTBrapaA | ATCTTTTTAC AAAC TGAA | TT TTCTACCGGG TCTGATGTAC A | ATGCTAGTC      |     |
| ConsePGIintUNTRRH1   | ATCTTTTTAC AAAC TGAA | TT TTCTACCGGG TCTGATGTAC A | ATGCTAGTC      |     |
| PGIBo-EM:AF258277    | ATCTTTTTAC AAAC TGAA | TT TTCTACCGGG TCTGATGTAC A | ATGCTAGTC      |     |
| PGIBra-EM:AF258278   | ACCTTTTTAC AAAC TGAA | AT GTCTACCGGG TCTGATGTAC A | ATGCTAGTC      |     |
| consePGIintUNTBolera | ATCTTTTTAC AAAC TGAA | TT TTCTACCGGG TCTGATGTAC A | ATGCTAGTC      |     |
| consePGIintUNTR2000  | ATCTTTT.AC AAAC TGAA | TT TTCTACCGGG TCTGATGTAC A | ATGCTAGTC      |     |
| Consensus            | atctttttac aaactgaa  | tt ttctaccggg tctgatgtac a | atgctAGTC      |     |

Figure 14 (a)

|                       |                       |   |
|-----------------------|-----------------------|---|
| 201                   | PGI int U --->        | 250   |
| consePGIintUNTDrakka  | CTGT                  | CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGT |
| consensWesrPGI        | CTGT                  | CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGT |
| consePGIintUNTR113    | CTGT                  | CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGT |
| consePGIintUNTRBrapaA | CTGT                  | CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGT |
| ConsePGIintUNTRRH1    | CTGT                  | CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGT |
| PGIBo-EM:AF258277     | CTGT                  | CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGT |
| PGIBra-EM:AF258278    | CTGT                  | CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGT |
| consePGIintUNTBolera  | CTGT                  | CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGT |
| consePGIintUNTR2000   | CTGT                  | CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGT |
| Consensus             | ctgtcagcac            | taatcttgc ggtatg aatt tgtgattaaa tttgtttgt        |
| 251                   |                       | 300   |
| consePGIintUNTDrakka  | TGTGACTCTT            | T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA       |
| consensWesrPGI        | TGTGACTCTT            | T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA       |
| consePGIintUNTR113    | TGCGACTCTT            | T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA       |
| consePGIintUNTRBrapaA | TGCGACTCTT            | T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA       |
| ConsePGIintUNTRRH1    | TGCGACTCTT            | T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA       |
| PGIBo-EM:AF258277     | TGTGACTCTT            | T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA       |
| PGIBra-EM:AF258278    | TGTGACTCTT            | TTCTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA       |
| consePGIintUNTBolera  | TG.GACTCTT            | T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA       |
| consePGIintUNTR2000   | TGTGACTCTT            | T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA       |
| Consensus             | tg.gactctt            | t.cttcattg ttcgTTTTcg tacaataaac cgaatgtata       |
|                       | e                     | e3  |
| 301                   | <---                  | PGIol antL 341 350                                |
| consePGIintUNTDrakka  | ATCTTTTTAC AAAC TGAA  | TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC              |
| consensWesrPGI        | ATCTTTTTAC AAAC TGAA  | TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC              |
| consePGIintUNTR113    | ATCTTTTTAC AAAC TGAA  | TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC              |
| consePGIintUNTRBrapaA | ATCTTTTTAC AAAC TGAA  | TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC              |
| ConsePGIintUNTRRH1    | ATCTTTTTAC AAAC TGAA  | TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC              |
| PGIBo-EM:AF258277     | ATCTTTTTAC AAAC TGAA  | TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC              |
| PGIBra-EM:AF258278    | ACCTTTTTAC AAAC TGAA  | AT GTCTACCGGG TCTGATGTAC A ATGCTAGTC              |
| consePGIintUNTBolera  | ATCTTTTTAC AAAC TGAA  | TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC              |
| consePGIintUNTR2000   | ATCTTTTT.AC AAAC TGAA | TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC              |
| Consensus             | atctttttac aaactgaa   | tt ttctaccggg tctgatgtac a atgctAGTC              |
|                       | e                     |   |
| 351                   |                       | 400   |
| consePGIintUNTDrakka  | TCCATGTTCT TGGGGATCAT | GATTTATTTT CTACATGTAT TCAGACAGTA                  |
| consensWesrPGI        | TCCATGTTCT TGGGGATCAT | GATTTATTTT CT.CATGTAT TCAGACAGTA                  |
| consePGIintUNTR113    | TCCATGTTCT TGGGGATCAT | GATTTATTTT CTACATGTGT TCAGCCAGTA                  |
| consePGIintUNTRBrapaA | TCCATGTTCT TGGGGATCAT | GATTTATTTT CTACATGTGT TCAGCCAGTA                  |
| ConsePGIintUNTRRH1    | TCCATGTTCT TGGGGATCAT | GATTTATTTT CTACATGTAT TCAGACAGTA                  |
| PGIBo-EM:AF258277     | TCCATGTTCT TGGGGATCAT | GATTTATTTT CTACATGTAT TCAGACAGTA                  |
| PGIBra-EM:AF258278    | TCCATGTTCT TGGGGATCAT | GATTTATTTT CTACATGTAT TCAGACAGTA                  |
| consePGIintUNTBolera  | TCCATGTTCT TGGGGATCAT | GATTTATTTT CTACATGTAT TCAGACAGTA                  |
| consePGIintUNTR2000   | TCCATGTTCT TGGGGATCAT | GATTTATTTT CTACATGTAT TCAGACAGTA                  |
| Consensus             | TCCATGTTCT TGGGGATCAT | GATTTATTTT CTaCATGTat TCAGACAGTA                  |
|                       |                       | e5 e6   |
| 401                   |                       | 450   |
| consePGIintUNTDrakka  | CAGAAGAAAG TGTTCAAAAC | TCTGGATGTT TTAATTTACA GTTAGTGGAG                  |
| consensWesrPGI        | CAGAAGAAAG TGTTCAAAAC | TCTGGATGTT TTAATTTACA GTTAGTGGAG                  |
| consePGIintUNTR113    | CAGAAGAAAG TGTTTAAAC  | TCTGGATGTT TTAATTTACA GTTAGTGGAG                  |
| consePGIintUNTRBrapaA | CAGAAGAAAG TGTTTAAAC  | TCTGGATGTT TTAATTTACA GTTAGTGGAG                  |
| ConsePGIintUNTRRH1    | CAGAAGAAAG TGTTTAAAC  | TCTGGATGTT TTAATTTACA GTTAGTGGAG                  |
| PGIBo-EM:AF258277     | CAGAAGAAAG TATTTAAAC  | TCTGGATGTT TTAATTTACA GTTAGTGGAG                  |
| PGIBra-EM:AF258278    | CAGAAGAAA TGTTTAAAC   | TCTGGATGTT TTGATTTACA GTTAGTGGAG                  |
| consePGIintUNTBolera  | CAGAAGAAAG TGTTCAAAAC | TCTGGATGTT TTAATTTACA GTTAGTGGAG                  |
| consePGIintUNTR2000   | CAGAAGAAAG TGTTCAAAAC | TCTGGATGTT TTAATTTACA GTTAGTGGAG                  |
| Consensus             | CAGAAGAAAg TgTTCAAAAC | TCTGGATGTT TTAATTTACA GTTAGTGGAG                  |
|                       | e7                    | e   |

Figure 14 (b)

|                      |            |                                |            |            |             |     |
|----------------------|------------|--------------------------------|------------|------------|-------------|-----|
|                      | 451        | end of Data Base PGI sequences |            |            |             | 500 |
| consePGIintUNTDrakka | AAGTTCGGCA | TTGATCCGAA                     | CAATGCATTT | GCATTTTGGG | ACTGGGTTGG  |     |
| consensWesrPGI       | AAGTTCGGCA | TTGATCCGAA                     | CAATGCATTT | GCATTTTGGG | ACTGGGTTGG  |     |
| consePGIintUNTR113   | AAGTTCGGCA | TTGATCCGAA                     | CAATGCATTT | GCATTTTGGG | ACTGGGTTGG  |     |
| consePGIintUNTBrapaA | AAGTTCGGCA | TTGATCCGAA                     | CAATGCATTT | GCATTTTGGG | ACTGGGTTGG  |     |
| ConsePGIintUNTRRH1   | AAGTTCGGCA | TTGATCCGAA                     | CAATGCATTT | GCATTTTGGG | ACTGGGTTGG  |     |
| PGIBo-EM:AF258277    | AAGTTCGGCA | TTGATCC...                     | .....      | .....      | .....       |     |
| PGIBra-EM:AF258278   | AAGTTCGGCA | TTGATCCGAA                     | CAA.....   | .....      | .....       |     |
| consePGIintUNTBolera | AAGTTCGGCA | TTGATCCGAA                     | CAATGCATTT | GCATTTTGGG | ACTGGGTTGG  |     |
| consePGIintUNTR2000  | AAGTTCGGCA | TTGATCCGAA                     | CAATGCATTT | GCATTTTGGG | ACTGGGTTGG  |     |
| Consensus            | AAGTTCGGCA | TTGATCCgaa                     | caatgcattt | gcattttggg | actgggttgg  |     |
|                      | 501        |                                |            |            |             | 550 |
| consePGIintUNTDrakka | TGGAAGGTAC | AGTGGTAAGT                     | GCTTGTTTAT | TTGGTTGTAT | AAATTTCTCG  |     |
| consensWesrPGI       | TGGAAGGTAC | AGTGGTAAGT                     | GCTTGTTTAT | TTGGTTGTAT | AAATTTCTCG  |     |
| consePGIintUNTR113   | TGGAAGGTAC | AGTGGTAAGT                     | GCTTGTTTAT | TTGGTTGTAT | TAATTTCTCA  |     |
| consePGIintUNTBrapaA | TGGAAGGTAC | AGTGGTAAGT                     | GCTTGTTTAT | TTGGTTGTAT | TAATTTCTCA  |     |
| ConsePGIintUNTRRH1   | TGGAAGGTAC | AGTGGTAAGT                     | GCTTGTTTAT | TTGGTTGTAT | TAATTTCTCA  |     |
| PGIBo-EM:AF258277    | .....      | .....                          | .....      | .....      | .....       |     |
| PGIBra-EM:AF258278   | .....      | .....                          | .....      | .....      | .....       |     |
| consePGIintUNTBolera | TGGAAGGTAC | AGTGGTAAGT                     | GCTTGTTTAT | TTGGTTGTAT | AAATTTCTCG  |     |
| consePGIintUNTR2000  | TGGAAGGTAC | AGTGGTAAGT                     | GCTTGTTTAT | TTGGTTGTAT | AAATTTCTCG  |     |
| Consensus            | tggaaggtac | agtggtaagt                     | gcttgtttat | ttggttgtat | .aatttctc.  |     |
|                      |            |                                |            |            | 8           | 9   |
|                      | 551        |                                |            |            |             | 600 |
| consePGIintUNTDrakka | TCCATTTCCG | CTTGCTTAGT                     | GTATAACTGA | AATTCTTTTG | CAGTTTGCAG  |     |
| consensWesrPGI       | TCCATTTCCG | CTTGCTTAGT                     | GTATAACTGA | AATTCTTTTG | CAGTTTGCAG  |     |
| consePGIintUNTR113   | TCCATATCCG | CTTGCTTAGT                     | TTATAACTGA | AATTCTTTTG | CAGTTTGCAG  |     |
| consePGIintUNTBrapaA | TCCATATCCG | CTTGCTTAGT                     | TTATAACTGA | AATTCTTTTG | CAGTTTGCAG  |     |
| ConsePGIintUNTRRH1   | TCCATATCCG | CTTGCTTAGT                     | TTATAACTGA | AATTCTTTTG | CAGTTTGCAG  |     |
| PGIBo-EM:AF258277    | .....      | .....                          | .....      | .....      | .....       |     |
| PGIBra-EM:AF258278   | .....      | .....                          | .....      | .....      | .....       |     |
| consePGIintUNTBolera | TCCATTTCCG | CTTGCTTAGT                     | GTATAACTGA | AATTCTTTTG | CAGTTTGCAG  |     |
| consePGIintUNTR2000  | TCCATTTCCG | CTTGCTTAGT                     | GTATAACTGA | AATTCTTTTG | CAGTTTGCAG  |     |
| Consensus            | tccat.tccg | cttgcttagt                     | .tataactga | aattcttttg | cagtttgcag  |     |
|                      | 10         |                                | 11         |            |             |     |
|                      | 601        |                                |            |            |             | 650 |
| consePGIintUNTDrakka | TGCTGTTGGA | GTCTTACCAT                     | TGTCTCTACA | GTATGGCTTC | TCTGTGGTTG  |     |
| consensWesrPGI       | TGCTGTTGGA | GTCTTACCAT                     | TGTCTCTACA | GTATGGCTTC | TCTGTGGTTG  |     |
| consePGIintUNTR113   | TGCTGTTGGA | GTCTTACCAT                     | TGTCTCTACA | GTATGGCTTC | TCCGTGGTTG  |     |
| consePGIintUNTBrapaA | TGCTGTTGGA | GTCTTACCAT                     | TGTCTCTACA | GTATGGCTTC | TCCGTGGTTG  |     |
| ConsePGIintUNTRRH1   | TGCTGTTGGA | GTCTTACCAT                     | TGTCTCTACA | GTATGGCTTC | TCCGTGGTTG  |     |
| PGIBo-EM:AF258277    | .....      | .....                          | .....      | .....      | .....       |     |
| PGIBra-EM:AF258278   | .....      | .....                          | .....      | .....      | .....       |     |
| consePGIintUNTBolera | TGCTGTTGGA | GTCTTACCAT                     | TGTCTCTACA | GTATGGCTTC | TCTGTGGTTG  |     |
| consePGIintUNTR2000  | TGCTGTTGGA | GTCTTACCAT                     | TGTCTCTACA | GTATGGCTTC | TCTGTGGTTG  |     |
| Consensus            | tgctgttgga | gtcttaccat                     | tgtctctaca | gtatggcttc | tc.tgtggttg |     |
|                      |            |                                |            |            | 12          |     |
|                      | 651        |                                |            |            |             | 700 |
| consePGIintUNTDrakka | AGAAGTACGG | TACCTTCTAC                     | TTTATAGCC  | ATCTCATAAA | ATGCTTTAGG  |     |
| consensWesrPGI       | AGAAGTACGG | TACCTTCTAC                     | TTTATAGCC  | ATCTCATAAA | ATGCTTTAGG  |     |
| consePGIintUNTR113   | AGAAGTACGG | TACCTTCTAC                     | TTTATTAGCC | ATCTCATAAA | ATGCTTTGGG  |     |
| consePGIintUNTBrapaA | AGAAGTACGG | TACCTTCTAC                     | TTTATTAGCC | ATCTCATAAA | ATGCTTTGGG  |     |
| ConsePGIintUNTRRH1   | AGAAGTACGG | TACCTTCTAC                     | TTTATTAGCC | ATCTCATAAA | ATGCTTTGGG  |     |
| PGIBo-EM:AF258277    | .....      | .....                          | .....      | .....      | .....       |     |
| PGIBra-EM:AF258278   | .....      | .....                          | .....      | .....      | .....       |     |
| consePGIintUNTBolera | AGAAGTACGG | TACCTTCTAC                     | TTTATAGCC  | ATCTCATAAA | A.GTCTTTAGG |     |
| consePGIintUNTR2000  | AGAAGTACGG | TACCTTCTAC                     | TTTATAGCC  | ATCTCATAAA | ATGCTTTAGG  |     |
| Consensus            | agaagtacgg | taccttctac                     | tttat.agcc | atctcataaa | atgtctt.gg  |     |
|                      |            |                                | 13         |            | 14          |     |



Figure 14 (c)

|                      |            |            |            |            |            |
|----------------------|------------|------------|------------|------------|------------|
|                      | 701        |            |            |            | 750        |
| consePGIintUNTDrakka | CATATTCTTT | CTATTTTATT | TTCCTCTTAA | TGATTTCTTC | TTTTTTTTAT |
| consensWesrPGI       | CATATTCTTT | CTATTTTATT | TTCCTCTTAA | TGATTTCTTC | TTTTTTTTAT |
| consePGIintUNTR113   | CATATTCTTT | CTATTTTATT | TTCCTCTGAA | TGATTTCTTC | TCTTTTAT.. |
| consePGIintUNTBrapaA | CATATTCTTT | CTATTTTATT | TTCCTCTGAA | TGATTTCTTC | TCTTTTAT.. |
| ConsePGIintUNTRRH1   | CATATTCTTT | CTATTTTATT | TTCCTCTGAA | TGATTTCTTC | TCTTTTAT.. |
| PGIBo-EM:AF258277    | .....      | .....      | .....      | .....      | .....      |
| PGIBra-EM:AF258278   | .....      | .....      | .....      | .....      | .....      |
| consePGIintUNTBolera | CATATTCTTT | CTATTTTATT | TTCCTCTTAA | TGATTTCTTC | TTTTTTTA.. |
| consePGIintUNTR2000  | CATATTCTTT | CTATTTTATT | TCCCTCTTAA | TGATTTCTTC | TTTTTTTTAT |
| Consensus            | catattcttt | ctattttatt | ttcctctaa  | tgatttcttc | t.tttt.t.. |
|                      |            |            | 15         |            | 16 17      |
|                      | 751        |            |            |            | 800        |
| consePGIintUNTDrakka | TGCATTCCCG | TTTTATTTTC | AAAAGTTGTT | ACTGTCTCTA | AATCAAGAAG |
| consensWesrPGI       | TGCATTCCCG | TTTTATTTTC | AAAAGTTGTT | ACTGTCTCTA | AATCAAGAAG |
| consePGIintUNTR113   | TGCATTCCCG | TTTTATTTTC | AAAAGTTGTC | ACTGTCTCTA | AATCAAGAAG |
| consePGIintUNTBrapaA | TGCATTCCCG | TTTTATTTTC | AAAAGTTGTC | ACTGTCTCTA | AATCAAGAAG |
| ConsePGIintUNTRRH1   | TGCATTCCCG | TTTTATTTTC | AAAAGTTGTC | ACTGTCTCTA | AATCAAGAAG |
| PGIBo-EM:AF258277    | .....      | .....      | .....      | .....      | .....      |
| PGIBra-EM:AF258278   | .....      | .....      | .....      | .....      | .....      |
| consePGIintUNTBolera | TGCATTCCCG | TTTTATTT.C | AAAAGTTGTC | CGGCCCCCTA | AACCAAGAAG |
| consePGIintUNTR2000  | TGCATTCCCG | TTTTATTTTC | AAAAGTTGTT | ACTGTCTCTA | AATCAAGAAG |
| Consensus            | tgattcccg  | ttttattttc | aaaagttgt. | actgtctcta | aatcaagaag |
|                      |            |            |            |            |            |
|                      | 801        |            |            |            | 850        |
| consePGIintUNTDrakka | AAACCTTCTT | AGTAGATCCA | GCTGATATTC | AGCCTTTTCT | AAATTGGACT |
| consensWesrPGI       | AAACCTTCTT | AGTAGATCCA | GCTGATATTC | AGCCTTTTCT | AAATTGGACT |
| consePGIintUNTR113   | AAACCTTCTT | AGTAGATCCA | GTTGATATTC | AGCCTTTTCT | AAATTGGACT |
| consePGIintUNTBrapaA | AAACCTTCTT | AGTAGATCCA | G.TGATATTC | AGCCTTTTCT | AAATTGGACT |
| ConsePGIintUNTRRH1   | AAACCTTCTT | AGTAGATCCA | GTTGATATTC | AGCCTTTTCT | AAATTGGACT |
| PGIBo-EM:AF258277    | .....      | .....      | .....      | .....      | .....      |
| PGIBra-EM:AF258278   | .....      | .....      | .....      | .....      | .....      |
| consePGIintUNTBolera | AAACCTTCTT | AGGA...CCA | GA...CTCC  | ACCCTTTTCT | AAATTGGACT |
| consePGIintUNTR2000  | AAACCTTCTT | AGTAGATCCA | GCTGATATTC | AGCCTTTTCT | AAATTGGACT |
| Consensus            | aaaccttctt | agtagatcca | g.tgatattc | agcctttt.t | aaattggact |
|                      |            |            | 18         |            | 19         |
|                      | 851        |            |            |            | 900        |
| consePGIintUNTDrakka | GCAGGTTTTT | AAA.GGGAGC | TTCAAGCATT | GATAGCATT  | TCCAGTCCCC |
| consensWesrPGI       | GCAGGTTTTT | AAA.GGGAGC | TTCAAGCATT | GATAGCATT  | TCCAGTCCAC |
| consePGIintUNTR113   | GCAGGTTTTT | AAA.GGGAGC | TTCAAGCATT | GATCAGCATT | TCCAGTCC.. |
| consePGIintUNTBrapaA | GCAGGTTTTT | AAA.GGGAGC | TTCAAGCATT | GATCAGCATT | TCCAGTCC.. |
| ConsePGIintUNTRRH1   | GCAGGTTTTT | AAA.GGGAGC | TTCAAGCATT | GATCAGCATT | TCCAGTCCAC |
| PGIBo-EM:AF258277    | .....      | .....      | .....      | .....      | .....      |
| PGIBra-EM:AF258278   | .....      | .....      | .....      | .....      | .....      |
| consePGIintUNTBolera | GCAGGTTTTT | AAA.GGGGGC | TTCAAGCATT | GATAGCATT  | TCCAGTCCAC |
| consePGIintUNTR2000  | GCAGGTTTTT | AAACGGGAGC | TTCAAGCATT | GATAGCATT  | TCCAGTCCAC |
| Consensus            | gcagggtttt | aaa.gggagc | ttcaagcatt | gatagcatt  | tccagtcc.c |
|                      |            |            |            | 20         |            |
|                      | 901        |            |            |            | 950        |
| consePGIintUNTDrakka | ACC.GTTTGA | GAAGAATATA | CCCGTGAGTT | GCATTAGTT  | GTGTGATTAT |
| consensWesrPGI       | ACC.GTTTGA | GAAGAATATA | CCCGTGAGTT | GCATTAGTT. | GTGTGATTAT |
| consePGIintUNTR113   | .CCCGTTTGA | GAAGAATATA | CCCGTGAGTT | GCATTAGTT. | ..GTGATTAT |
| consePGIintUNTBrapaA | .CCCGTTTGA | GAAGAATATA | CCCGTGAGTT | GCATTAGTT. | GTGTGATTAT |
| ConsePGIintUNTRRH1   | ACC.GTTTGA | GAAGAATATA | CCCGTGAGTT | GCATTAGTT. | GTGTGATTAT |
| PGIBo-EM:AF258277    | .....      | .....      | .....      | .....      | .....      |
| PGIBra-EM:AF258278   | .....      | .....      | .....      | .....      | .....      |
| consePGIintUNTBolera | ACCCGTTTGA | GAAGAATATA | CCCGTGAGTT | GCATTAGTT. | GTGTGATTAT |
| consePGIintUNTR2000  | ACC.GTTTGA | GAAGAATATA | CCCGTGAGTT | GCATTAGTT. | GTGTGATTAT |
| Consensus            | acc.gtttga | gaagaatata | cccgtagt   | gcattagt   | gtgtgattat |

Figure 14 (d)

|                      |             |                        |                                  |
|----------------------|-------------|------------------------|----------------------------------|
|                      | 951         |                        | 1000                             |
| consePGIintUNTDrakka | ACAGTTTTTC  | TTGTCTTTTT             | GCTATGCCCA TCAACACTAG AAGATTCGTG |
| consensWesrPGI       | ACAGTTTT.C  | TTGTCTTTTT.            | GCTATGTCCA TCAACACTAG A.GATTCGTG |
| consePGIintUNTR113   | ACAGTTTT.C  | TTGCCTTTTT             | GCTAT..AGG GCAAC.CTAG A.GATTCATG |
| consePGIintUNTBrapaA | ACAGTTTT.C  | TTGTCTTTTT.            | GCTATG.TCA TCAAC.CTAG A.GATTCATG |
| ConsePGIintUNTRRH1   | ACAGTTTT.C  | TTGTCTTTTT             | GCTAT...AT GCAACCCTAG ..GATTCATG |
| PGIBo-EM:AF258277    | .....       | .....                  | .....                            |
| PGIBra-EM:AF258278   | .....       | .....                  | .....                            |
| consePGIintUNTBolera | ACAGTTTT.C  | TTGTCTTTTT             | GCTAG..TGA TCAAC.CTAG A.GATTCGTG |
| consePGIintUNTR2000  | ACAGTTTT.C  | TTGTCTTTTT             | GCTATGTCCA TCAACACTAG A.GATTCGTG |
| Consensus            | acagtttt.c  | ttgtcttttt             | gctat....a tcaac.ctag a.gattc.tg |
|                      |             |                        | 21                               |
|                      | 1001        |                        | 1050                             |
| consePGIintUNTDrakka | AAGTTATTAG  | TGTAGCCAAC             | GCCTAGGGGG AGGTTGGTTG GCTGTTTTGG |
| consensWesrPGI       | AAGTTATTAG  | TGTAGTCAAC             | GCA.....                         |
| consePGIintUNTR113   | AAGTTATTAG  | TGTAGTCAAC             | GCAGAGGAGA G..TTCCTG ACGG.....   |
| consePGIintUNTBrapaA | AAGTTATTAG  | TGTAGTCAAC             | GCAGAGTGAG AGG.TGATTG .....      |
| ConsePGIintUNTRRH1   | AAGTTATTAG  | TGTAGTCAAC             | GCAGAGGAGG AGATGGTT.. .....      |
| PGIBo-EM:AF258277    | .....       | .....                  | .....                            |
| PGIBra-EM:AF258278   | .....       | .....                  | .....                            |
| consePGIintUNTBolera | AAGTTATTAG  | TGTAGTCAAC             | GCATAGGAGG AGC.....              |
| consePGIintUNTR2000  | AAGTTATTAG  | TGTAGTCAAC             | GCATAGGGAG AGGTGAT.GG TGACTTTTGG |
| Consensus            | aagttattag  | tgtagtcaac             | gca.agg.g. .g.....               |
|                      | 1051        | 1076                   |                                  |
| consePGIintUNTDrakka | ACGTTTTTCAC | GTGCTCCGGG             | GGGTTTTTGG GGACCAAACC CCCAAC     |
| consensWesrPGI       | .....       | .....                  | .....                            |
| consePGIintUNTR113   | .....       | .....                  | .....                            |
| consePGIintUNTBrapaA | .....       | .....                  | .....                            |
| ConsePGIintUNTRRH1   | .....       | .....                  | .....                            |
| PGIBo-EM:AF258277    | .....       | .....                  | .....                            |
| PGIBra-EM:AF258278   | .....       | .....                  | .....                            |
| consePGIintUNTBolera | .....       | .....                  | .....                            |
| consePGIintUNTR2000  | ACGATTT     | CAG GTGCTTTAGG GTTATTG | .....                            |

Figure 15 (a)

|                     |                   |             |  |
|---------------------|-------------------|-------------|--|
|                     | 51                |             | 100  |
| EMBH44836anti       | .....             | .....       | .....  |
| GCP18-5CP418L-Sams  | .....             | .....       | .....  |
| GCP18-2CP418L-Wes   | .....             | .....       | .....  |
| GCP18-4CP418L-R2000 | .....             | .....       | CP418L...                                    |
| conse129ba1-Drak    | .....             | AAACAAATCA  | AAATTCTAAA TTTCTCCA                          |
| GCPS18-129Sam-ba2   | .....             | AAAC TATGTA | ACAAAAATCA AAATTGTAAA TTTCTCCA               |
| GCPR18-3129R211-ba2 | .....             | .....       | AA CCAAAAATCC AAATTGTAAA TTTCTCCCT.          |
| GCP18-10129R20-ba2  | .....             | .....       | CAAAATCCA AAATTGTAAA TTTCT.CCT               |
| Consensus           | .....             | .....       | .....  |
|                     | 101               |             | 150  |
| EMBH44836anti       | .....             | .....       | .....  |
| GCP18-5CP418L-Sams  | .....             | .....       | AT A.CATTTTCT GTAA                           |
| GCP18-2CP418L-Wes   | .....             | AGG T.AT    | A.CATTTTCT GTAA                              |
| GCP18-4CP418L-R2000 | .....             | AGG TCAT    | A.CATTTTCT GTAA                              |
| conse129ba1-Drak    | TCACAAAGGAC       | CTACAGAATA  | GAGTTATCAT AACATTT CT GTAA                   |
| GCPS18-129Sam-ba2   | TCGTAAAGGAC       | CTACAGAATA  | GAGTTATCAT AACATTTTCT G AA                   |
| GCPR18-3129R211-ba2 | TGGTAACGGC        | CTCAAAAA.A  | GAGGTATCAA AAC.TTTTCT GT.A                   |
| GCP18-10129R20-ba2  | TGGTTACCGC        | C.CAAAAA.A  | AAGGT..CAA AACTT.TCCG GTAA                   |
| Consensus           | .....             | .....       | .....  |
|                     | 151               |             | 200  |
| EMBH44836anti       | .....             | .....       | .....  |
| GCP18-5CP418L-Sams  | .TATTTCCAT        | CAAAATGA..  | .CTAGAGAAC AGCAGTTCTT ATAACATTAT             |
| GCP18-2CP418L-Wes   | .TATTTCCAT        | CAAAATGA..  | .CTAGAGAAC AG.AGTTCTT ATAACATTAT             |
| GCP18-4CP418L-R2000 | ATATTTCCAT        | CAAAATGA..  | .CTAGAGAAC AG.AGTTCTT ATAACATTAT             |
| conse129ba1-Drak    | ATATTTCCAT        | CAAAATGA..  | .CTAGAGAAC AG.AGTTCTT ATAACATTAT             |
| GCPS18-129Sam-ba2   | ATGTTTCCAT        | CAAAATGA    | CTATCGAAC ATAATTAAT ATA.CATTTT               |
| GCPR18-3129R211-ba2 | ATGTTTCCAT        | CAAAATG.    | CTATCGGAC ATAATTAAT ATAAC.TTCT               |
| GCP18-10129R20-ba2  | ATGTTTCCAT        | CAAAATG.    | CTTCGGA.C ATAATTAAT ATAAC.TTCT               |
| Consensus           | ATGTTTCCCT        | CAAA.TGG    | CTTCGGA.C ATAATTAAA A...CATTCT               |
|                     | 201               |             | 250  |
| EMBH44836anti       | .....             | .....       | .....  |
| GCP18-5CP418L-Sams  | CTGTAAA TG.TTCCAA | CAAAA CCACT | ACATAGCAGAGTTC .TTATAACAT                    |
| GCP18-2CP418L-Wes   | CTGTAAA TG.TTCCAA | CAAAA CCACT | ACATAGCAGAGTTC ATTATAACAT                    |
| GCP18-4CP418L-R2000 | CTGTAAA TG.TTCCAA | CAAAA CCACT | ACATAGCAGAGTTC .TTATAACAT                    |
| conse129ba1-Drak    | CTGTAAA TG.TTCCAA | CAAAA CCACT | ACATAGCAGAGTTC .TTATAACAT                    |
| GCPS18-129Sam-ba2   | CTG.AAAAT.AATTCCT | CAAAA.TTA.  | .CATTTTC TTACAA.A.                           |
| GCPR18-3129R211-ba2 | CTG.AAAAT.AATTCCT | CAAAA.TTA.  | .CATTTTC TTACAA.A.                           |
| GCP18-10129R20-ba2  | CTG.AAA.TAATTCCT  | CAAAA.TTA.  | .CATTTTC TTACAA.A.                           |
| Consensus           | .....             | .....       | .....  |
|                     | 251               |             | 300  |
| EMBH44836anti       | .....             | .....       | .....CTATACC                                 |
| GCP18-5CP418L-Sams  | TGTCTGT.AA        | ATGTCCAATC  | AAAACCACTA CAGAACAAAG CTCCTATAAC             |
| GCP18-2CP418L-Wes   | TGTCTGT.AA        | ATGTCCAATC  | AAAACCACTA CAGAACAAAG CTCCTATAAC             |
| GCP18-4CP418L-R2000 | TGTCTGT.AA        | ATGTCCAATC  | AAAACCACTA CAGAACAAAG CTCCTATAAC             |
| conse129ba1-Drak    | TGTCTGT.AA        | ATGTCCAATC  | AAAACCACTA CAGAACAAAG CTCCTATAAC             |
| GCPS18-129Sam-ba2   | TGTTTC...         | .....       | .....CATCAAAATG AGACTCCA.G                   |
| GCPR18-3129R211-ba2 | TGTTTC...         | .....       | .....CATCAAAATG AGACTCCA.G                   |
| GCP18-10129R20-ba2  | TGTTTC...         | .....       | .....CATCAAAATG AGACTCCA.G                   |
| Consensus           | tttctgt.aa        | tggtttccatc | aaaatgacta tcgaacataa ttaatAtaac             |
|                     | 301               |             | 350  |
| EMBH44836anti       | A                 | TTGTTT      | ATACAAAGTT TCACT AAAT CTACAAACTT CCCCCGTAAA  |
| GCP18-5CP418L-Sams  | A                 | TTGTTT      | ATACAAAGTTT .CACT AAAT CTACAAACTT TCCCCGTAAA |
| GCP18-2CP418L-Wes   | A                 | TTGTTT      | ATACAAAGTT TCACT AAAT CTACAAACTT TCCCCGTAAA  |
| GCP18-4CP418L-R2000 | A                 | TTGTTT      | ATACAAAGTTT .CACT AAAT CTACAAACTT TCCCCGTAAA |
| conse129ba1-Drak    | A.                | TGTTT       | ATACAAAGTT TCACT AAAT CTACAAACTT TCCCCGTAAA  |
| GCPS18-129Sam-ba2   | AAC.CAGTTC        | TTGCATAGTT  | TCACTTAAAT CTACAAACTT TC.....                |
| GCPR18-3129R211-ba2 | AACACAGTTC        | TTGCATAGTT  | TCACT.AAAT CTACAAACTT TC.....                |
| GCP18-10129R20-ba2  | A.CCCAGTTC        | TTGCATAGTT  | TC.CT.AAAT CTTCAAACTT TC.....                |
| Consensus           | .....             | .....       | .....  |

Figure 15 (b)

|                     |  |                                  |     |
|---------------------|--|----------------------------------|-----|
|                     | 351  |                                  | 400 |
| EMBH44836anti       | TGAGCTTAAT ATCACCCAA.                                  | GATGTTTCA ATCAGAT AAA GAGTAACGAC |     |
| GCP18-5CP418L-Sams  | TGAGCTTAAT ATCACCCAAA                                  | GATGTTTCA ATCAGAT AAA GAGTAACGAC |     |
| GCP18-2CP418L-Wes   | TGAGCTTAAT ATCACCCAAA                                  | GATGTTTCA ATCAGAT AAA GAGTAACGAC |     |
| GCP18-4CP418L-R2000 | TGAGCTTAAT ATCACCCAAA                                  | GATGTTTCA ATCAGAT AAA GAGTAACGAC |     |
| conse129ba1-Drak    | TGAGCTTAAT ATCACCCAAA                                  | GATGTTTCA ATCAGAT AAA GAGTA.CGAC |     |
| GCPS18-129Sam-ba2   | .....AAT CTTATCTTAA                                    | G.TTATCAC ATCAGAT GAA GA.....    |     |
| GCPR18-3129R211-ba2 | .....AAT CTTATCTTAA                                    | G.TTATCAC ATCAGAT GAA GA.....    |     |
| GCP18-10129R20-ba2  | .....AAT CTTATCTTAA                                    | G.TTATCAC ATCAGAT GAA GA.....    |     |
| Consensus           | .....AAT CTTATCTTAA                                    | G.TTATCAC ATCAGAT GAA GA.....    |     |
|                     | 401  |                                  |     |
| EMBH44836anti       | ATCGTTTTGA GATTAGAACA AA                               |                                  |     |
| GCP18-5CP418L-Sams  | ATCGTTTTGA GATTAGAACA AA                               |                                  |     |
| GCP18-2CP418L-Wes   | ATCGTTTTGA GATTAGAACA AA                               |                                  |     |
| GCP18-4CP418L-R2000 | ATCGTTTTGA GATTAGAACA AA                               |                                  |     |
| conse129ba1-Drak    | ATCGTTTTGA GATTAGAACA AA                               |                                  |     |
| GCPS18-129Sam-ba2   | ....GAGC AA  |                                  |     |
| GCPR18-3129R211-ba2 | ....GAGC AA  |                                  |     |
| GCP18-10129R20-ba2  | ....GAGC A.  |                                  |     |
| Consensus           | ....GAGC A.  |                                  |     |
|                     | 431  |                                  | 480 |
| EMBH44836anti       | CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC |                                  |     |
| GCP18-5CP418L-Sams  | CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC |                                  |     |
| GCP18-2CP418L-Wes   | CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC |                                  |     |
| GCP18-4CP418L-R2000 | CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC |                                  |     |
| conse129ba1-Drak    | CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC |                                  |     |
| GCPS18-129Sam-ba2   | CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC |                                  |     |
| GCPR18-3129R211-ba2 | CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC |                                  |     |
| GCP18-10129R20-ba2  | CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC |                                  |     |
| Consensus           | .t.aa.ctta c.tagagtga t.tgaggagt.aggctcggtg ccagc.gagc |                                  |     |
|                     | 481  |                                  | 530 |
| EMBH44836anti       | TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGACCTG AGACAACCGT  |                                  |     |
| GCP18-5CP418L-Sams  | TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGACCTG AGACAACCGT  |                                  |     |
| GCP18-2CP418L-Wes   | TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGACCTG AGACAACCGT  |                                  |     |
| GCP18-4CP418L-R2000 | TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGACCTG AGACAACCGT  |                                  |     |
| conse129ba1-Drak    | TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGACCTG AGACAACCGT  |                                  |     |
| GCPS18-129Sam-ba2   | TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGACCTG AGACAACCGT  |                                  |     |
| GCPR18-3129R211-ba2 | TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGACCTG AGACAACCGT  |                                  |     |
| GCP18-10129R20-ba2  | TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGACCTG AGACAACCGT  |                                  |     |
| Consensus           | tagctctctc ctccgcctca tgaagcatct g.tgacactg agacaaccgt |                                  |     |
|                     | 531  |                                  | 580 |
| EMBH44836anti       | GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA |                                  |     |
| GCP18-5CP418L-Sams  | GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA |                                  |     |
| GCP18-2CP418L-Wes   | GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA |                                  |     |
| GCP18-4CP418L-R2000 | GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA |                                  |     |
| conse129ba1-Drak    | GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA |                                  |     |
| GCPS18-129Sam-ba2   | GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA |                                  |     |
| GCPR18-3129R211-ba2 | GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA |                                  |     |
| GCP18-10129R20-ba2  | GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA |                                  |     |
| Consensus           | gacgaaactt tccgatcacc gccaccagaa ttcgacgccg cgcacccgaa |                                  |     |
|                     | 581  |                                  | 630 |
| EMBH44836anti       | GGATCCGAAT CGGGAACCTG AGTGAACCCG AGCGATCCCG GGAGTGCGAC |                                  |     |
| GCP18-5CP418L-Sams  | GGATCCGAAT CGGGAACCTG AGTGAACCCG AGCGATCCCG GGAGTGCGAC |                                  |     |
| GCP18-2CP418L-Wes   | GGATCCGAAT CGGGAACCTG AGTGAACCCG AGCGATCCCG GGAGTGCGAC |                                  |     |
| GCP18-4CP418L-R2000 | GGATCCGAAT CGGGAACCTG AGTGAACCCG AGCGATCCCG GGAGTGCGAC |                                  |     |
| conse129ba1-Drak    | GGATCCGAAT CGGGAACCTG AGTGAACCCG AGCGATCCCG GGAGTGCGAC |                                  |     |
| GCPS18-129Sam-ba2   | GGATCCGAAT CGGGAACCTG AGTGAACCCG AGCGATCCCG GGAGTGCGAC |                                  |     |
| GCPR18-3129R211-ba2 | GGATCCGAAT CGGGAACCTG AGTGAACCCG AGCGATCCCG GGAGTGCGAC |                                  |     |
| GCP18-10129R20-ba2  | GGATCCGAAT CGGGAACCTG AGTGAACCCG AGCGATCCCG GGAGTGCGAC |                                  |     |
| Consensus           | ggatccgaat cgggaacttg agtgaaccg agcgatcccg ggagtgcgac  |                                  |     |

Figure 15 (c)

|                     |            |            |                                  |
|---------------------|------------|------------|----------------------------------|
|                     | 631        |            | 690                              |
| EMBH44836anti       | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT TCGACGAAGA GTGGAAGAGG |
| GCP18-5CP418L-Sams  | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT TCGACGAAGA GTGGAAGAGG |
| GCP18-2CP418L-Wes   | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT TCGACGAAGA GTGGAAGAGG |
| GCP18-4CP418L-R2000 | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT TCGACGAAGA GTGGAAGAGG |
| conse129ba1-Drak    | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT TCGACGAA.A GTGGAAGAGG |
| GCPS18-129Sam-ba2   | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT TCGACGAAGA GAGGAAGAGG |
| GCPR18-3129R211-ba2 | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT TCGACGAAGA GAGGAAGAGG |
| GCP18-10129R20-ba2  | GGAGCGATGG | GAAAAGAGAG | TGGCACGATT TCG.CGAAGA GAGGAAGAGG |
| Consensus           | ggagcg.tgg | .aaaagagag | tggcacgatt tcgacgaaga g.ggaagagg |

|                     |            |             |                                  |
|---------------------|------------|-------------|----------------------------------|
|                     | 691        |             | 740                              |
| EMBH44836anti       | AGAGGGTGGT | GGATAAACTC  | GCGTATGATC AAGTTCGTCA TCGTCCTGAT |
| GCP18-5CP418L-Sams  | AGAGGGTGGT | GGATAAACTC  | GCGTATGATC AAGTTCGTCA TCGTCCTGAT |
| GCP18-2CP418L-Wes   | AGAGGGTGGT | GGATAAACTC  | GCGTATGATC AAGTTCGTCA TCGTCCTGAT |
| GCP18-4CP418L-R2000 | AGAGGGTGGT | GGATAAACTC  | GCGTATGATC AAGTTCGTCA TCGTCCTGAT |
| conse129ba1-Drak    | AGAGGGTGGT | GGATAAACTC  | GCGTATGATC AAGTTCGTCA TCGTCCTGAT |
| GCPS18-129Sam-ba2   | AGAGGGTGGT | GGATAAACTC  | GCGTATGATC AAGTTCGTCA TCGTCCTGAT |
| GCPR18-3129R211-ba2 | AGAGG.TGGT | GGATAAACTC  | GCGTATGATC AAGTTCGTCA TCGTCCTGAA |
| GCP18-10129R20-ba2  | AGAGGGTGGT | GGATAAACTC  | GCGTATGATC AAGTTCGTCA TCGTCCTGAA |
| Consensus           | agaggggtgg | ggataaaactc | gcgtatgatc aagttcgtca tcgtcctga. |

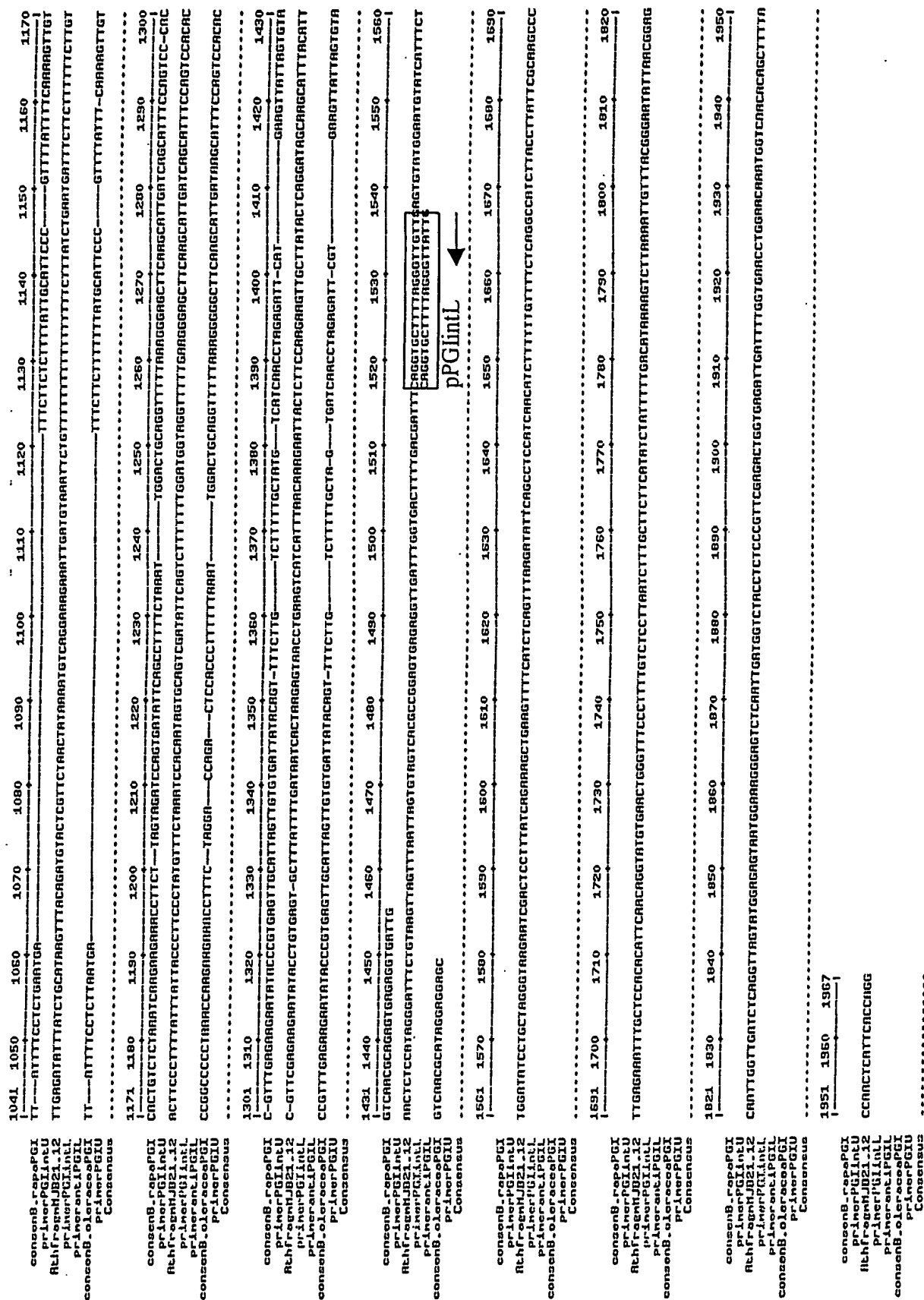
|                     |            |             |                                  |      |
|---------------------|------------|-------------|----------------------------------|------|
|                     | 741        | pSG129antiU | 790                              | 800  |
| EMBH44836anti       | TGCCGCCATT | TTTTTTGTCA  | GGGCGCTCTG TGGCTTAGAA GTTTCCGATG |      |
| GCP18-5CP418L-Sams  | TGCCGCCATT | TTTTTTGTCA  | GGGCGCTCTG TGGCTTAGAA GTTTCCGATG |      |
| GCP18-2CP418L-Wes   | TGCCGCCATT | TTTTTTGTCA  | GGGCGCTCTG TGGCTTAGAA GTTTCCGATG |      |
| GCP18-4CP418L-R2000 | TGCCGCCATT | TTTTTTGTCA  | GGGCGCTCTG TGGCTTAGAA GTTTCCGATG |      |
| conse129ba1-Drak    | TGCCGCCATT | TTTTTTGTCA  | GGGCGCTCTG TGGCTTAGAA GTTTCCGATG |      |
| GCPS18-129Sam-ba2   | TGCCGCCATT | TTTTTTGTCA  | GGGCGCTCTG TGGCTTAGAA GTTTCCGATG |      |
| GCPR18-3129R211-ba2 | TGCCGCC... | TTTTTTGTCA  | GGGCGCTCTG TGGCTTAGAA GTTTCCGATG |      |
| GCP18-10129R20-ba2  | TGCC..CAT. | TTTTTTGTCA  | GGGCGCTCTG TGGCTTAGAA GTTTCCGATG |      |
| Consensus           | tgccgccat. | .tt.....c.  | .gg.gc.c.g                       | .... |

|                     |                                |
|---------------------|--------------------------------|
|                     | 791                            |
| EMBH44836anti       | TCAATGAAC A GTGACACGAC GAAATGC |
| GCP18-5CP418L-Sams  | TCAATGAAC AGAAT...TC CGGG...   |
| GCP18-2CP418L-Wes   | CCAATGAACA AGATTATTC CGATG..   |
| GCP18-4CP418L-R2000 | .....                          |
| conse129ba1-Drak    | .....                          |

[illegible]

## Figure 16<sup>BIS</sup>



[illegible]



## Figure 17<sup>BIS</sup>

